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Global Governance of Genomic Pathogen Surveillance

Opportunities and Challenges

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What Is Genomic Pathogen Surveillance?

Genomic pathogen surveillance is a powerful complement to public-health infrastructure that can help researchers and public-health officials inform pandemic and epidemic preparedness, drug discovery and management of endemic diseases.

Genomic surveillance is a multi-step process. It begins with a strategy to identify and collect pathogen samples, informed by research and public-health priorities. Researchers or clinical technicians use machines to process these pathogens and yield their genetic code, the *sequence*. Powerful computational tools must then assemble and analyse this raw sequence data in a standardised manner. *Genomic surveillance* is the process of using this prepared, whole-genome data, alongside many previously observed pathogen sequences, to identify the emergence and spread of pathogens.

The immediate value of genomic surveillance lies in recognising changes in the genome that indicate the appearance of new lineages – some of concern – and mutations that produce changes in a pathogen's behaviour, such as resistance to vaccines or therapeutic drugs. These classes of information enable recognising and tracking outbreaks, identifying drug resistance and improving surveillance of infectious diseases. Thus, genomic pathogen surveillance could help enhance the medical management of patients, empower improved local public-health interventions and strengthen global responses to infectious diseases, particularly for epidemics and pandemics.

Pathogen monitoring has traditionally relied on international academic-researcher networks sharing unexpected phenomena within a relatively narrow set of patient samples. In the past two decades, however, developments in both genomic sequencing and data-sharing infrastructure

have significantly changed these processes, enabling researchers and clinical technicians to systematically sequence and analyse large sets of samples from the broad population.

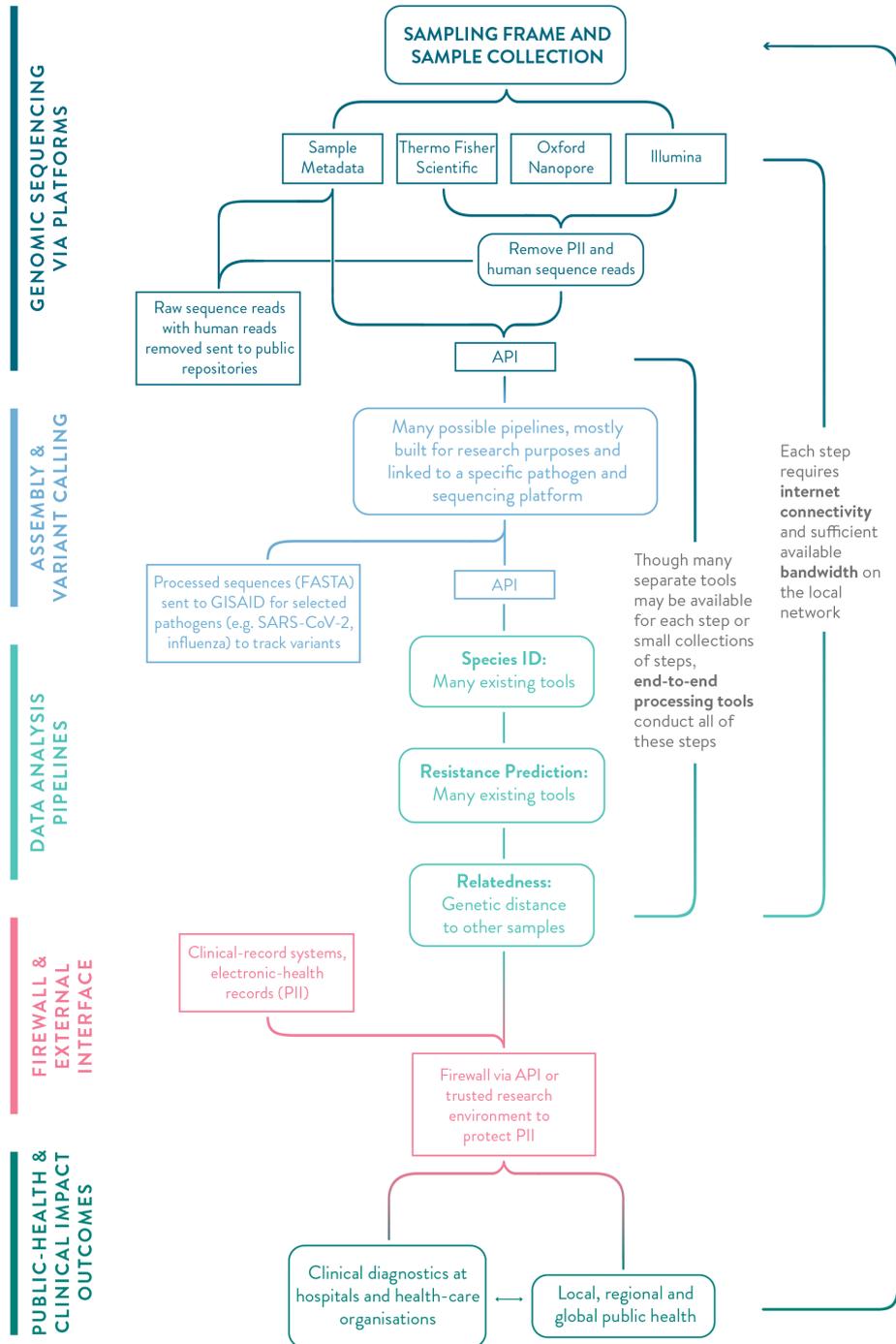
These technologies include:

- **Next-generation sequencers** to rapidly generate raw genomic data from a biological sample.
- **Processing software** that cleans and analyses these data sets in a standardised manner.
- **Cloud-based data-storage systems** to store and share data efficiently and securely, at scale.
- **Data-visualisation tools** to aid analysis, identify trends and communicate findings to decision-makers.
- **Global databases and repositories**, such as the Global Initiative on Sharing Avian Influenza Data (GISAID), that allow researchers to share genomic data internationally and identify trends and genomic mutations.

These technologies represent a link in the chain from swab sample to public-health policy decision at both the national and international levels (Figure 1). These advances – coupled with coordination on standard-setting, funding and governance activities at local, national and global levels – will enable the international community to scale and systematise genomic-surveillance capabilities for use in regular public-health monitoring of pandemic, epidemic and endemic diseases.

Figure 1

SEQUENCE DATA PROCESSING AND ANALYSIS FOR GLOBAL GENOMIC SURVEILLANCE OF ALL PATHOGENS



API refers to "application programming interface"
 GISAID refers to Global Initiative on Sharing Avian Influenza Data
 PII refers to "personally identifiable information"

International Governance Challenges in Genomic Surveillance

Technological capability is necessary but not sufficient. At the international level, effective genomic pathogen surveillance depends on the timely sharing of genomic data and standardised analytical processes that allow for valid comparisons across internationally sourced samples.

The current practice for international genomic data sharing is largely unsystematised, from sampling to data sharing. Historically, researchers' sampling strategy – the decisions they make around how to collect biological samples to study – was based on convenience. They primarily relied on local human and animal participants because it was impracticable or unnecessary for their purposes to sample more broadly. While national public-health institutions are increasingly introducing [more systematic genomic-sampling initiatives](#), these are primarily focused on human – not pathogen – genomic monitoring. What's more, genomic data remain non-representative on the global level as most available data come from high-income countries (HICs) in Europe and North America. These non-representative sampling strategies risk introducing bias into epidemiological results about pathogen spread or impact. The World Health Organisation's (WHO) recently issued [genomic-surveillance sampling strategy](#) highlights globally representative sampling as a key objective.

Similarly, in data processing, a lack of technical standards has limited the use of genomic sequencing in public health. As genomic sequencing has typically been a matter of academic research rather than public-health infrastructure, researchers maintain and apply bespoke data-analysis tools tailored to their specific research questions. Therefore, it is difficult to compare data from different sources and systematically process them for public-health purposes. They have likely been processed differently, using different tools, reference standards and assumptions that would impact joint analysis.

Finally, in terms of data sharing, data owners voluntarily contribute some or all of their samples on a case-by-case basis, sharing data in raw-genome or locally pre-processed formats. They are shared either through informal academic lab networks or on repositories such as GISAID or the European Molecular Biology Laboratory's European Bioinformatics Institute (EMBL-EBI). More systematised governance will be necessary to expand these data-sharing exchanges so that public-health agencies can regularly benefit and ensure that data sharers are protected and adequately incentivised.

This practice is partly driven by a long history of ethical and geopolitical concerns that disincentivise systematic genomic-data sharing. International and academic governance initiatives over the past 20 years – including the 2008 [introduction of the GISAID repository](#) and the 2010 [Nagoya Protocol](#) on access and benefit-sharing of genomic samples – have gone a long way towards addressing ethical and technical concerns. However, despite the solid successes and important role of the genomic-surveillance ecosystem in the overall pandemic response, the pandemic exposed persistent weaknesses in technological standards, global genomic-sequencing capacity and governance that the global community will need to address collectively.

The past two years have seen a wide range of stakeholders addressing this issue, introducing a proliferation of technological and governance initiatives to build on the successes of the Covid-19 genomic-surveillance effort and close the gaps that still exist. Most notably, the WHO's recently announced [Hub for Pandemic and Epidemic Intelligence](#) in Berlin and its [ten-year genomic-surveillance strategy](#) represent a significant step in the design and oversight of an effective and equitable global genomic-surveillance system. Adopting some of these technologies and initiatives will go a long way to addressing these challenges, balancing the risk that a proliferation of solutions exacerbates standardisation and governance problems. It is essential to converge as a global community, including governments, researchers, local clinicians, non-governmental organisations (NGOs) and the new WHO Hub, to cement best practices, set standards and establish governance mechanisms that build on the Nagoya principles to accelerate the pace of change.

GOVERNANCE IN RESPONSE TO ETHICAL AND GEOPOLITICAL CONCERNS

The data sharing that enables international genomic data-surveillance networks to perform effectively raises ethical and geopolitical concerns, given the sensitivity and intrinsic value of genomic data.

The first concern is that researchers and life-sciences companies from HICs harvest data shared by low- and middle-income country (LMIC) participants without the recognition, compensation and local investment they deserve. While there are clear, widespread benefits of HIC researchers and the pharmaceutical industry collaborating in data analysis and vaccine or treatment development, it is essential to do so in a manner that recognises and builds out local capabilities. This issue came to a head in 2009 in the aftermath of the H5N1 (avian flu) pandemic, when [Indonesian officials stopped](#) sharing genomic data with WHO reference labs because HIC researchers and pharmaceutical companies exploited the data without proper consultation or compensation to Indonesian researchers who generated the data. This included the concern that the companies would use the data to develop vaccines that would then be sold to Indonesia at exorbitant prices. Indeed, early data repositories such as EMBL, DNA Data Bank of Japan (DDBJ) and GenBank were developed for data to be shared and used freely. Notably, [GISAID](#) was developed, in part, out of a desire to recognise data sharers, enable attribution as research collaborators, and ultimately protect and incentivise their data sharing. The data-access protections it has put in place have benefitted and [built trust among data sharers](#).

The Nagoya Protocol on genetic-data access and benefit-sharing addresses this concern, extending the international Convention on Biological Diversity to bind stakeholders in signatory countries to domestic-access measures and benefit-sharing obligations when genomic resources are shared internationally. These obligations include informed-consent procedures to protect sharers, mutually agreed contracting and dispute-resolution terms, terms to establish justice procedures and monitoring requirements to hold resource beneficiaries responsible for resources passed on to third parties.

Analysis in the *Guardian* recently argued that Covid-19 was the first pandemic since the Nagoya Protocol was agreed upon and therefore is the first test case. Still, [while countries shared SARS-CoV-2 resources freely](#) throughout the pandemic “demanding nothing in return”, beneficiaries have not fully respected the spirit of the agreement. They have not shared the benefits of these resources in terms of vaccine distribution or intellectual property (IP). According to legal scholar Mark Eccleston-Turner, “We’re treating pathogen sharing as a common good [under Nagoya], but we’re

not treating vaccines and medical countermeasures as a common good,” as vaccine IP has been held privately by developers. This discrepancy arises partly because it is [unclear whether Nagoya covers pathogens](#) (it explicitly covers biodiversity). Further, the burden has been on sample-generating countries to demand and specify benefit-sharing terms *ex-ante* even though it may be difficult to appreciate the full extent of these in advance. Concern that countries would withhold virus samples to extract significant compensation limits action on both points.

In addition, data sharers often face significant disincentives, particularly during pandemics. South Africa openly shared data identifying the Omicron variant of concern during the Covid-19 pandemic but experienced adverse economic impact and stigma because of countries’ travel warnings and initial location-centric framing (labelling it the “South African variant”). Similarly, as references to an “Indian variant” emerged on social media, the [Indian government wrote](#) to social-media companies to request that they take down this wording, fearing it would cause undue harm to the country’s reputation.

This geopolitical problem requires governance solutions that [actively create incentives for data sharing](#) to ensure the most important data – indicating potential outbreaks of concern – are systematically shared and indeed such sharing rewarded. [South African researchers were discouraged](#) from sharing follow-on data that demonstrated Omicron was milder than other variants because their findings were treated with outside scepticism. These reputational costs are further disincentives to systematic data sharing. As an example of global governance efforts to overcome these disincentives, the [WHO promulgated](#) a Greek letter-naming convention to avoid “stigmatising and discriminatory” place-based names.

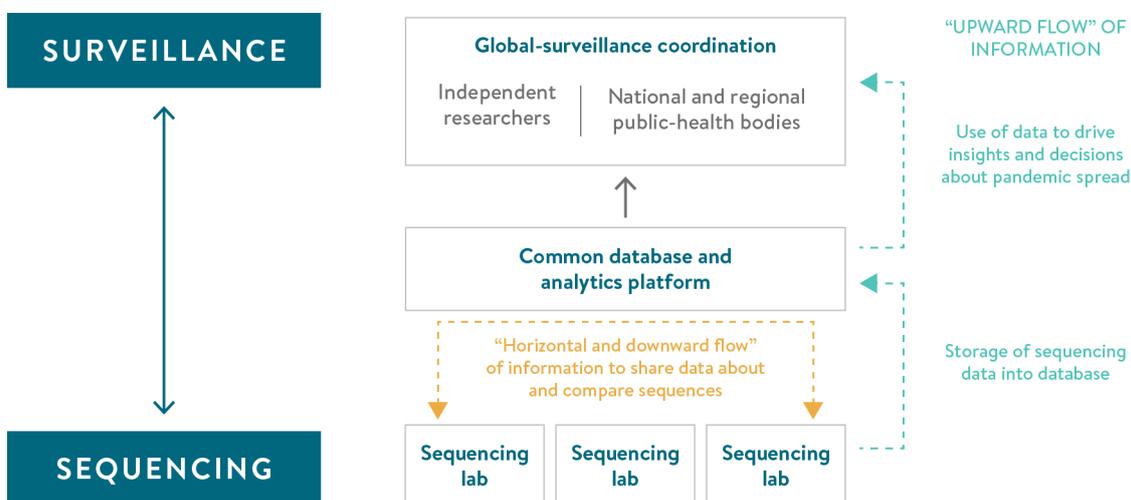
STANDARD-SETTING ACTIVITY

In addition to these ethical responses, the global genomic-surveillance community needs technical and practice standards to coordinate activity effectively and ensure data are accurate and comparable at the global level. Research consortia, international organisations and NGOs have recognised this need and have been actively proposing standards for all or part of the genomic pathogen-surveillance architecture.

A [global genomic-surveillance network](#) engages many organisations and technologies (Figure 2). As genomic sequencing becomes increasingly integrated into routine public-health monitoring, it is more important than ever to have technical and governance standards to ensure these information flows are timely, accurate and coherent across all settings.

Figure 2

A ROADMAP OF THE INSTITUTIONS AND TECHNOLOGIES TRANSLATING GENOMIC-SEQUENCING ACTIVITIES INTO A GLOBAL GENOMIC-SURVEILLANCE NETWORK



Source: GHSC Illustration

For example, the Rockefeller Foundation, in partnership with Stanford researchers Marc Salit and Arend Sidow, recently issued a working paper called “Building Towards a Standards Architecture for Pathogen Genomic Surveillance”. The paper defines a process model that specifies the genomic-surveillance workflow and calls for leading institutions to take on a governance role to set and encourage the use of global standards at each stage of the process.

This proposal reflects similar calls from academic researchers who work closely with public-health agencies. [Allison Black and colleagues](#) in *Nature* propose ten recommendations for open genomic analysis for public health, notably standardised pipelines for data processing, analysis and visualisation, as well as metadata for analysis and comparison across samples, sites and public-health bodies. Similarly, the Public Health Alliance for Genomic Epidemiology (PHA4GE), including some of the above researchers, has also proposed [standards for SARS-CoV-2 genomic-sequence metadata](#), the contextual information necessary to analyse, compare, and track pathogen spread and variants, which could serve more broadly as a framework for metadata publication in repositories.

SCALING GENOMIC-SEQUENCING CAPACITY AROUND THE WORLD

For genomic-surveillance infrastructure to be useful, it needs to be accompanied by widespread genomic sequencing around the world. However, as it stands, genomic-sequencing capacity remains patchy, and stark differences exist between richer and poorer countries. More than 70 per cent of genomic-sequencing capacity in Africa is [concentrated in just five countries](#).

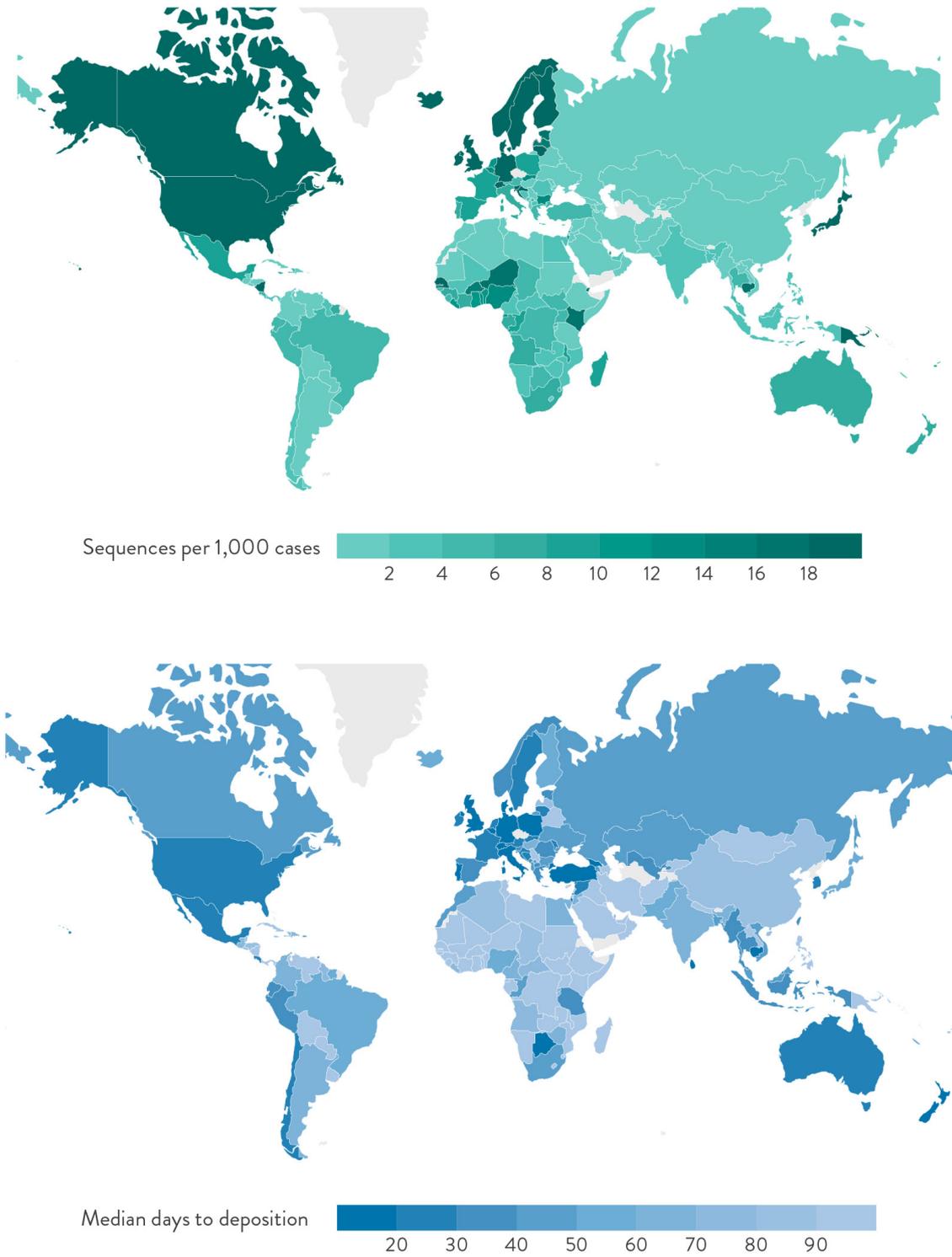
Observed levels of sequencing activity during the Covid-19 pandemic show global genomic-surveillance capabilities and capacity in practice. During the pandemic, from [January 2020 to March 2021](#), there were no SARS-CoV-2 sequences available for 49 countries (a quarter of the world's nations). And up to December 2021, [more than 80 per cent](#) of the more than 5 million SARS-CoV-2 genomes uploaded to the GISAID database came from Europe and North America. Between [February 2020 to March 2021](#), HICs sequenced an average of 1.81 per cent of Covid-19 cases, while LICs sequenced 0.11 per cent. Although many countries have the basic equipment for genomic sequencing, their surveillance of SARS-CoV-2 was often low for other reasons.

Genomic-sequencing capabilities are limited by:

- A lack of equipment, including sequencing machines, and sufficient internet connectivity and network bandwidth.
- A lack of workforce and expertise.
- A global shortage of raw materials, such as the reagents needed to carry out the sequencing process. HICs [have been accused](#) of hoarding these materials, requiring global governance to coordinate the provision of these rival goods.
- Coordination and logistics. For example, although the United States has the equipment and expertise for sequencing, many diagnostic labs do not share their samples with researchers or undertake genomic sequencing due to the extra labour or storage required. A failure of coordination also meant that it took the US an [average of 72 days](#) to process and share each genetic sequence, compared with 23 days in the UK.
- A lack of diagnostic capacity. For genomes to be sequenced, cases need to be reported and samples taken.

Figure 3

GENOMIC SEQUENCING THROUGHOUT THE COVID-19 PANDEMIC



Source: COVID CG

From a technical standpoint, [expanding on-the-ground genomic-sequencing capabilities is essential](#). This includes training adequate numbers of staff and investing in equipment, internet connectivity and other necessary resources to conduct sequencing work.

However, genomic-sequencing capacity alone is not sufficient. Targeted system design is also required to increase sequencing efficiency tailored to the local context, including a sampling frame and sampling strategy that allow officials to identify and sequence possible cases. Although South Africa has significantly less genomic-sequencing capacity than countries such as Brazil, the UK and India, it [identified Beta and Omicron more quickly](#), mainly because it approached sequencing more strategically. The [WHO's ten-year global genomic-surveillance strategy](#) underscores the need for a value-for-money approach to expanding capacity in ways that are economical, efficient, effective, equitable and ethical, “as high throughput sequencing and bioinformatics for pathogens with pandemic and epidemic potential are cost-intensive and remain out of reach for many”. Ultimately, these efforts require increased funding, including national contributions and international contributions from HICs, international consortia like the G20, NGOs and private companies in this space. International HIC stakeholders must recognise the collective benefits from increased capacity at the global level and the ethical responsibility to extend these capabilities to LMIC contexts.

Oversight and Coordination

The current global pathogen genomic-surveillance infrastructure rests on two decades of governance activity, including formal standard setting and ethics protocols at the national and international levels.

Sir Jeremy Farrar submitted [a proposal for an equitable global genomics-surveillance network](#) as part of the UK's 2021 G7 presidency. It sets out the necessary components of an international architecture to monitor pathogen emergence and mutation. In addition to the necessary technologies described earlier, these represent the institutional capabilities and governance mechanisms that will underpin global genomic surveillance, including:

- A “mesh network” of pre-existing expert centres.
- Core infrastructure to sequence, analyse and share data.
- A modernised sampling, governance and ethics framework.
- New data-driven tools to fight disease.
- Global normative leadership to set values and governance principles for international data sharing.

Over the past 18 months, the WHO has launched a set of governance activities that represent an important step towards an effective, global pandemic- and epidemic-surveillance network. These include:

- Opening negotiations on a pandemic treaty to set legally binding commitments for surveillance, integrated processes and tasks, and public- and private-sector support during a pandemic response (March 2022).
- A [ten-year strategy for global genomic pathogen surveillance](#) (March 2022).
- Announcement of the [WHO Hub for Pandemic and Epidemic Intelligence based in Berlin](#) (September 2021).
- The [WHO BioHub System](#) for international biological-sample sharing (2021).

The WHO's hub is led by Dr Chikwe Ihekweazu, previously Director-General of the Nigeria Centre for Disease Control (NCDC). It will focus on the [following missions](#):

- Enhance methods for accessing multiple data sources vital to generating signals and insights on disease emergence, evolution and impact.
- Develop state-of-the-art tools to process, analyse and model data for detection, assessment and response.
- Provide the WHO, its member states and partners with these tools to underpin better, faster decisions on how to address outbreak signals and events.
- Connect and catalyse institutions and networks developing disease-outbreak solutions for the present and future.

These missions will help establish the hub's role as a convening institution and help drive the global genomic-surveillance community towards a coherent network.

Finally, NGOs have played an important role in this space, providing funding and convening activities, and drawing attention to the importance of standard setting and governance. For example, the Rockefeller Foundation has been increasingly active in this area, issuing a series of [grants](#) and a standards-architecture proposal as the basis for its new [Pandemic Prevention Institute](#). In 2021, it provided GISAID with [its largest grant to date](#), a [\\$5 million grant](#) between 2021 and 2024, to advance GISAID's pathogen data-sharing platform and tools. Similarly, the Bill & Melinda Gates Foundation (BMGF) has built a [funding stream for vaccine development and surveillance](#). BMGF is making several grants to support genomic-surveillance activity, most notably a grant to the Africa Centres for Disease Control and Prevention to help create the \$100 million Africa Pathogen Genomics Initiative and a \$1 million grant to India's CSIR-Institute of Genomics and Integrative Biology. Bill Gates's latest book, [How to Prevent the Next Pandemic](#), also calls public attention to the importance of global genomic surveillance and makes key recommendations to shine both a [floodlight on potential threats and a laser focus on the response](#).

Conclusion

The clear impact of genomic surveillance during the Covid-19 pandemic demonstrates its value to academic research, clinical care and public health at the national and international levels. It is now more important than ever to continue the Covid-era investment in the technical infrastructure and public-health decision-making processes for genomic surveillance. We must complement this investment with the institutional governance and technical standard-setting activities necessary to incentivise timely, ethical, accurate and coherent data sharing across a global genomic-surveillance network.

The upcoming G20 summit in Bali is an opportune moment to make these commitments, building on the WHO's new Hub for Pandemic and Epidemic Intelligence and its Global Genomic Surveillance Strategy. G20 countries should first invest in genomic-sequencing capacity – building out technological capability and training clinical personnel to carry out local sampling – and in national-level public-health infrastructure to translate this capability into public-health decisions. G20 countries must also contribute in financial, technological and governance terms to global efforts; NGOs and international organisations have played an important financial and coordinating role in building genomic-surveillance capability in LMICs, but G20 countries must contribute to these global initiatives as well as to their national efforts. This must be undertaken with respect for the ethical impact of these initiatives, ensuring LMICs realise the benefits of their contributions and that research capabilities are built with LMIC academic partners. Finally, at this stage, it is important to strike a balance between experimentation and coordination – the many actors calling for standard setting is promising and given the important technological and governance steps (for example, the WHO's hub and strategy), it is essential to coalesce around a global framework for action.

Genomic pathogen surveillance will be an increasingly crucial component of our public-health infrastructure. The investments we make today – financially and in terms of global coordination – will help ensure the genomic-surveillance infrastructure we build will contribute to future pandemic and epidemic preparedness, drug discovery, and routine clinical diagnosis and care.

Annex: Governance Landscape

A detailed list of active organisations and initiatives in the global genomic pathogen surveillance ecosystem.

Organisation/Event	Date	Activity	Detail
Indonesia refuses to share H5N1 flu virus data	2007	Governance, Ethics	Indonesia refused to share H5N1 flu virus samples with the WHO, arguing WHO scientists and laboratories violated their own guidelines in managing the samples. The country stopped sending samples in January 2007 because it was concerned LMICs were providing valuable samples that companies in high-income countries could use freely to develop costly vaccines and treatments.
GISAID	2008	Technology, Repository	GISAID is an international, online repository of genomic-sequencing data. It was created in 2008 in response to data-sharing disincentives observed during the H5N1 outbreak on existing repositories (EMBL, DDBJ, GenBank). Most notably, this includes identifying contributors and allowing for acknowledgement of data owners.
Nagoya Protocol	2010	Governance, Ethics	The Nagoya Protocol on Access and Benefit Sharing (2010) is an international agreement governing the use of genetic resources that extends the 1992 Convention on Biological Diversity. It establishes access measures at the domestic level and benefit-sharing obligations when genetic resources are shared internationally.
EU COMBACTE-NET	2013	Network	The EU COMBACTE-NET consortium is a public–private partnership (PPP) clinical, lab and research network across Europe to facilitate data sharing in response to anti-microbial resistance (clinical testing of novel antibacterial drugs).

Organisation/Event	Date	Activity	Detail
European Centre for Disease Prevention and Control (ECDC)	2016	Governance, Standard Setting	The European CDC issued an expert opinion in 2016 on genomic sequencing for public health , including the strengths and weaknesses of its use for multi-country outbreak detection and monitoring, the outlook for standardisation across labs of genomic analysis for surveillance at the EU level, and a strategy and role for the ECDC for both tech development and public-health applications.
China Centre for Disease Prevention and Control (China CDC)	2017	Network, Local Example	An overview of China's 20-year history of applying genomic surveillance to monitor pathogens including SARS-CoV-2, H7N9 flu, MERS and Zika virus.
The Africa CDC Institute of Pathogen Genomics (IPG)	2019	Network, Standard Setting	The IPG constitutes a pan-African network of national public-health institutes, an academy to train on the use of next generation sequencers (NGS), an architecture of interoperable software packages for genomic-sequence bioinformatics, and the development of use cases and best practices for African public-health bodies. Africa CDC launched the \$100 million Africa Pathogen Genomics Initiative (Africa PGI) in 2020 within the IPG, with public, private, and non-profit partners including the US CDC and BMGF, to provide funding and technical assistance.
Field Epidemiology Training Program (FETP)	2019	Network, Training, Standard Setting, Capacity Building	The Field Epidemiology Training Program (FETP) is a collaboration between the US CDC and WHO to help over 100 countries build training programmes to support local epidemiological data collection and public-health response. This includes governance principles for a global Strategic Leadership Group to set standards for and implement local FETPs.
UNITAID	2019	Grant, Network, Repository	UNITAID and FIND , the global diagnostics alliance, partnered on a \$14 million grant to set up the Seq&Treat project to expand genomic-sequencing capability to monitor drug-resistant TB in Brazil, China, Georgia, India and South Africa. UNITAID, FIND and the WHO have contributed to the largest catalogue of TB bacteria mutations , which was released in 2021.
EU Versatile Emerging infectious disease Observatory (VEO)	2020	Network, Monitoring, Decision Support	The VEO consortium consists of 20 research partners across Europe, funded by the EU. It is a system for early warning, risk assessment and monitoring of emerging infectious diseases, including surveillance of pathogens pre- and post-spillover from animal cases into humans.

Organisation/Event	Date	Activity	Detail
European Bioinformatics Institute (EMBL-EBI) Covid-19 Data Portal	2020	Network, Repository, Technology, Standard Setting	The European Bioinformatics Institute (EMBL-EBI) is a longstanding repository managed by the European Molecular Biology Laboratory. EMBL-EBI maintains databases, including the Covid-19 Data Portal of viral and host sequences, and analytical tools and software , to help share and analyse genetic data from publicly funded research.
FIND	2020	Network, Ecosystem Mapping	FIND is a global alliance for diagnostics and was recently funded by the Rockefeller Foundation to carry out a mapping of existing global capacity for SARS-CoV-2 genomics surveillance .
Nigeria Centre for Disease Control (NCDC)	2020	Local Example, Capacity Building	The Nigeria CDC has built up significant genomic-sequencing capacity and contributes to SARS-CoV-2 genomic surveillance at the regional (Africa PGI) and international (GISAID) levels. Its most recent Director-General, Dr Chikwe Ihekweazu, was selected to head the new WHO Hub for Pandemic and Epidemic Intelligence.
Pan-American Health Organisation (PAHO)	2020	Network, Governance, Capacity Building	PAHO established a COVID-19 Genomic Surveillance Regional Network to strengthen participating labs' genomic-sequencing capacity and share these data with the global research community. It also supports the WHO's 2022 ten-year global genomic-surveillance strategy .
India	2020	Network, Grantee, Local Example	India is building out a genomic-surveillance network, especially in response to Covid-19, including the Indian SARS-CoV-2 Genomics Consortium bringing together the Ministry of Health, Council for Scientific and Industrial Research (CSIR), and Indian Council of Medical Research, and 38 labs across the country. The BMGF contributed \$1 million to the CSIR-Institute of Genomics and Integrative Biology, and the Rockefeller Foundation has issued a report calling for strengthening of India's genomic-surveillance ecosystem .
Wellcome Sanger Institute	2020	Network, Standard Setting, Technology, Research	Wellcome has traditionally played a central role in international lab networks sharing and analysing genomic data and maintains the Covid-19 Genomics Initiative . Recently, it joined the Covid-19 Genomics UK (COG UK) Consortium , a UK network to deliver sequencing capabilities to the NHS and UK government.

Organisation/Event	Date	Activity	Detail
World Economic Forum (WEF)	2020	Network Convening, Standard Setting (high level)	WEF has conducted various convening activities in the pathogen-surveillance space, including an initiative with Australian Genomics and Canada's Genomics4RD to create a high-level eight-step genomic data-consortium governance model . It has also issued a genomic data-policy-framework white paper . However, beyond this convening activity, it is unclear how deep their involvement is in this space.
Aga Khan Development Network	2021	Research, Network, Local Example	Aga Khan University has been working with the WHO and Pakistani public- and private-sector laboratories to establish a genomic-surveillance system to detect the Omicron variant of concern.
Bill & Melinda Gates Foundation (BMGF)	2021	Grants, Network Building, Local Examples	The Bill & Melinda Gates Foundation has built out a funding stream on surveillance . BMGF is making several grants to support genomic-surveillance activity, most notably a grant to the Africa CDC to help create the \$100 million Africa Pathogen Genomics Initiative and a \$1 million grant to India's CSIR-Institute of Genomics and Integrative Biology.
Global Fund	2021	Grants, Local Example	The Global Fund is an international partnership addressing AIDS, TB and malaria. The Global Fund has just issued a £37 million grant to FIND, the global alliance for diagnostics, to support tuberculosis prevention and control in India, including genome surveillance for TB and drug-resistant TB treatment monitoring.
Institut Pasteur	2021	Grants, Local Example	Institut Pasteur, in partnership with the French Development Agency (AFD), French National Research Institute for Sustainable Development (IRD), and ANRS (French agency for research on AIDS) and labs across 13 African countries, launched AFROSCREEN , a €10 million project to strengthen local genomic-sequencing capabilities and develop monitoring and response processes to control and limit the spread of variants.
International Association of National Public Health Institutes (IANPHI)	2021	Network Convening, Standard Setting, Decision Support	IANPHI has played a convening role among national public-health institutes to identify best practices, gaps, and strategies for regional and international collaboration in genomic surveillance. They have collated strategies from member NPHIs here .
Robert Koch Institute	2021	Research, Local Example, Network	Germany's Robert Koch Institute has been highly active in the genomic-surveillance networks for SARS-CoV-2 , including projects in Germany , Europe and African countries .

Organisation/Event	Date	Activity	Detail
The Rockefeller Foundation	2021	Grants, Network Building, Standard Setting	The Rockefeller Foundation is a US grantmaking institution that has recently created the Pandemic Prevention Institute. It partnered with the Pandemic Tracking Collective , a group of largely volunteer data collectors and analysts active during Covid-19. Rockefeller also recently issued a proposal for a global genomic-data-standards architecture in collaboration with two Stanford researchers. This includes standard-setting along the entire genomic surveillance pathway, including public-health-driven sampling strategies, sample collection and sequencing, sequence bioinformatics, data integration and access, and public-health knowledge development from resulting data.
UK Health Security Agency (HSA)	2021	Network, Technology, Local Example, Governance	Genomic surveillance is part of the UK HSA remit , including establishing the New Variant Assessment Platform (NVAP) . The NVAP will provide support in the UK and foreign countries to strengthen their genomic-sequencing capability, either through local networks or by sequencing and analysing samples in the UK.
Public Health Alliance for Genomic Epidemiology (PHA4GE)	2022	Research, Standard Setting	PHA4GE is a research coalition working on setting standards and improving the availability of bioinformatics tools in genomic epidemiology. It recently published a metadata specification package for SARS-CoV-2, which could serve as a framework for metadata publication in repositories more broadly.
ARTIC		Network, Research, Technology, Decision Support	The ARTIC network brings together UK researchers from the University of Birmingham, University of Edinburgh, University of Cambridge and the Wellcome Trust. It is developing an end-to-end system for viral data processing to inform public-health decision-making, based on highly portable nanopore sequencers.
NIH Fogarty International Center		Research, Network Convening	Fogarty is a US National Institute of Health centre conducting global health research. Fogarty facilitated international research networks to track the SARS-CoV-2 virus , including collaborating with and training LMIC scientists to sequence coronavirus genomes.



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